

COMBINED DECLARATION AND POWER OF ATTORNEY
FOR CONTINUATION-IN-PART APPLICATION

AS A BELOW-NAMED INVENTOR, I HEREBY DECLARE THAT:

My residence, post office address and citizenship are as stated below next to my name.

I believe I am the original, first and sole inventor (if only one name is listed below) or an original, first and joint inventor (if more than one name is listed below) of the subject matter which is claimed and for which a patent is sought on the invention entitled: MAMMALIAN CHEMOKINES; RECEPTORS; REAGENTS; USES, the specification of which

X is attached hereto
— was filed on

and assigned Serial No. and was amended on .

I HAVE REVIEWED AND UNDERSTAND THE CONTENTS OF THE ABOVE-IDENTIFIED SPECIFICATION, INCLUDING THE CLAIMS, AS AMENDED BY ANY AMENDMENT REFERRED TO ABOVE.

I acknowledge and understand that I am an individual who has a duty to disclose information which is material to the patentability of the claims of this application in accordance with Title 37, Code of Federal Regulations, §§ 1.56(a) and (b) which state:

"(a) A patent by its very nature is affected with a public interest. The public interest is best served, and the most effective patent examination occurs when, at the time an application is being examined, the Office is aware of and evaluates the teachings of all information material to patentability. Each individual associated with the filing and prosecution of a patent application has a duty of candor and good faith in dealing with the Office, which includes a duty to disclose to the Office all information known to that individual to be material to patentability as defined in this section. The duty to disclose information exists with respect to each pending claim until the claim is cancelled or withdrawn from consideration, or the application becomes abandoned. Information material to the patentability of a claim that is cancelled or withdrawn from consideration need not be submitted if the information is not material to the patentability of any claim remaining under consideration in the application. There is no duty to submit information which is not material to the patentability of any existing claim. The duty to disclose all information known to be material to patentability is deemed to be satisfied if all information known to be material to patentability of any claim issued in a patent was cited by the Office or submitted to the Office in the manner prescribed by §§ 1.97(b)-(d) and 1.98. However, no patent will be granted on an application in connection with which fraud on the Office was practiced or attempted or the duty of disclosure was violated through bad faith or intentional misconduct. The Office encourages applicants to carefully examine:

(1) prior art cited in search reports of a foreign patent office in a counterpart application, and

(2) the closest information over which individuals associated with the filing or prosecution of a patent application believe any pending claim patentably defines, to make sure that any material information contained therein is disclosed to the Office.

(b) Under this section, information is material to patentability when it is not cumulative to information already of record or being made of record in the application, and

(1) It establishes, by itself or in combination with other information, a prima facie case of unpatentability of a claim; or

(2) It refutes, or is inconsistent with, a position the applicant takes in:

(i) Opposing an argument of unpatentability relied on by the Office, or

(ii) Asserting an argument of patentability.

A prima facie case of unpatentability is established when the information compels a conclusion that a claim is unpatentable under the preponderance of evidence, burden-of-proof standard, giving each term in the claim its broadest reasonable construction consistent with the specification, and before any consideration is given to evidence which may be submitted in an attempt to establish a contrary conclusion of patentability."

I do not know and do not believe this invention was ever known or used in the United States of America before my or our invention thereof, or patented or described in any printed publication in any country before my or our invention thereof or more than one year prior to said application. This invention was not in public use or on sale in the United States of America more than one year prior to this application. This invention has not been patented or made the subject of an inventor's certificate issued before the date of this application in any country foreign to the United States of America on any application filed by me or my legal representatives or assigns more than six months prior to this application.

I hereby claim priority benefits under Title 35, United States Code § 119(e)(1) of any United States provisional application(s) for patent as indicated below and have also identified below any application for patent on this invention having a filing date before that of the application for patent on which priority is claimed:

<u>Application No.</u>	<u>Date of Filing (day/month/year)</u>	<u>Priority Claimed</u>
60/053,693	July 25, 1997	Yes <input checked="" type="checkbox"/> No <input type="checkbox"/>

I hereby claim the benefit under Title 35, United States Code, § 120 of any United States application(s) listed below, and, insofar as the subject matter of each of the claims of this application is not disclosed in the prior United States application in the manner provided by the first paragraph of Title 35, United States Code § 112, I acknowledge the duty to disclose material information as defined in Title 37, Code of Federal Regulations, § 1.56(a) and (b) set forth above which occurred between the filing date of the prior application and the national or PCT international filing date of this application:

Application Serial No.: 09/122,585

Filing Date: July 24, 1998

Status (patented, pending, abandoned): pending

I hereby appoint the following attorneys and agents to prosecute that application and to transact all business in the Patent and Trademark Office connected therewith and to file, to prosecute and to transact all business in connection with all patent applications directed to the invention:

Roberta L. Robins, Reg. No. 33,208
Dahna S. Pasternak, Reg. No. 41,411
Gary R. Fabian, Ph.D., Reg. No. 33,875
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Address all telephone calls to: Sheela Mohan-Peterson at (650) 852-9196.

This appointment, including the right to delegate this appointment, shall also apply to the same extent to any proceedings established by the Patent Cooperation Treaty.

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under § 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

Signature: _____

Date _____

Full Name Inventor: Joseph A. Hedrick

Citizenship: US

Residence: US

Post Office Address: 52-08 Quail Ridge Drive, Plainsboro NJ 08536

Signature: _____

Date _____

Full Name Inventor: Bernhard Homey

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Signature: _____

Date _____

Full Name Inventor: Alain Vicari

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Signature: _____

Date _____

Full Name Inventor: Monica Zepeda

Citizenship: US

Residence: US

Post Office Address: 4247 Calle Mejillones, San Diego, CA 92130

Signature: _____

Date _____

Full Name Inventor: Albert Zlotnik

Citizenship: US

Residence: US

Post Office Address: 507 Alger Drive, Palo Alto, CA 94036

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Hedrick, Joseph A.
Vicari, Alain P.
Zlotnik, Albert
- (ii) TITLE OF INVENTION: Mammalian Chemokines; Receptors;
Reagents; Uses
- (iii) NUMBER OF SEQUENCES: 10
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: DNAX Research Institute
(B) STREET: 901 California Avenue
(C) CITY: Palo Alto
(D) STATE: California
(E) COUNTRY: USA
(F) ZIP: 94304-1104
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: US
(B) FILING DATE: 24-JUL-1998
(C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Ching, Edwin P.
(B) REGISTRATION NUMBER: 34,090
(C) REFERENCE/DOCKET NUMBER: DX0757
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (650)852-9196
(B) TELEFAX: (650)496-1200

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 179 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 18..179

091069-0700

(x) PUBLICATION INFORMATION:

(H) DOCUMENT NUMBER: US 60/053,693

(I) FILING DATE: 25-JUL-1997

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

```
GTAAACCAC ACTATTC ATG CAA AAG GGT GTA GGG TTA CTG AGG ACA GTT      50
      Met Gln Lys Gly Val Gly Leu Leu Arg Thr Val
          1              5              10

CCC TTG GTA CCT TCA GTC TCT GGT CAG ATT GAC CTT TTG GTA CTG TGT      98
Pro Leu Val Pro Ser Val Ser Gly Gln Ile Asp Leu Leu Val Leu Cys
          15              20              25

ATG TGT ATA AAA ACG ACT ACT CCT CAT ATA TTT ATT TCT GAT TAT AAG      146
Met Cys Ile Lys Thr Thr Thr Pro His Ile Phe Ile Ser Asp Tyr Lys
          30              35              40

ATA ATA TAT TCT GGA AAA CAC TGG AAA ATA CAT      179
Ile Ile Tyr Ser Gly Lys His Trp Lys Ile His
          45              50
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(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 54 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```
Met Gln Lys Gly Val Gly Leu Leu Arg Thr Val Pro Leu Val Pro Ser
  1              5              10              15

Val Ser Gly Gln Ile Asp Leu Leu Val Leu Cys Met Cys Ile Lys Thr
          20              25              30

Thr Thr Pro His Ile Phe Ile Ser Asp Tyr Lys Ile Ile Tyr Ser Gly
          35              40              45

Lys His Trp Lys Ile His
          50
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(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1314 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 179..1171

(x) PUBLICATION INFORMATION:
(H) DOCUMENT NUMBER: US 60/053,693
(I) FILING DATE: 25-JUL-1997

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GTCTAAAACA	AAATACAACA	TTTCTTAAAT	ACACTGTTTC	CAGAAAGAGC	TATTTTAACA	60
GAAGCAACTC	AAAGATATCC	CTTCGACAGA	AGTGGAAGTG	CTGAAAAATG	CTCATCTCTC	120
ACACAGACTT	TTGATGGACA	GGAGTTTCTA	AGTATCATGC	CTACCAACAA	GCTGTAAA	178
ATG ATC ACC CTG AAC AAT CAA GAT CAA CCT GTC CCT TTT AAC AGC TCA						226
Met Ile Thr Leu Asn Asn Gln Asp Gln Pro Val Pro Phe Asn Ser Ser						
1 5 10 15						
CAT CCA GAT GAA TAC AAA ATT GCA GCC CTT GTC TTC TAT AGC TGT ATC						274
His Pro Asp Glu Tyr Lys Ile Ala Ala Leu Val Phe Tyr Ser Cys Ile						
20 25 30						
TTC ATA ATT GGA TTA TTT GTT AAC ATC ACT GCA TTA TGG GTT TTC AGT						322
Phe Ile Ile Gly Leu Phe Val Asn Ile Thr Ala Leu Trp Val Phe Ser						
35 40 45						
TGT ACC ACC AAG AAG AGA ACC ACG GTA ACC ATC TAT ATG ATG AAT GTG						370
Cys Thr Thr Lys Lys Arg Thr Thr Val Thr Ile Tyr Met Met Asn Val						
50 55 60						
GCA TTA GTG GAC TTG ATA TTT ATA ATG ACT TTA CCC TTT CGA ATG TTT						418
Ala Leu Val Asp Leu Ile Phe Ile Met Thr Leu Pro Phe Arg Met Phe						
65 70 75 80						
TAT TAT GCA AAA GAT GCA TGG CCA TTT GGA GAG TAC TTC TGC CAG ATT						466
Tyr Tyr Ala Lys Asp Ala Trp Pro Phe Gly Glu Tyr Phe Cys Gln Ile						
85 90 95						
ATT GGA GCT CTC ACA GTG TTT TAC CCA AGC ATT GCT TTA TGG CTT CTT						514
Ile Gly Ala Leu Thr Val Phe Tyr Pro Ser Ile Ala Leu Trp Leu Leu						
100 105 110						
GCC TTT ATT AGT GCT GAC AGA TAC ATG GCC ATT GTA CAG CCG AAG TAC						562
Ala Phe Ile Ser Ala Asp Arg Tyr Met Ala Ile Val Gln Pro Lys Tyr						
115 120 125						
GCC AAA GAA CTT AAA AAC ACG TGC AAA GCC GTG CTG GCG TGT GTG GGA						610
Ala Lys Glu Leu Lys Asn Thr Cys Lys Ala Val Leu Ala Cys Val Gly						
130 135 140						
GTC TGG ATA ATG ACC CTG ACC ACG ACC ACC CCT CTG CTA CTG CTC TAT						658
Val Trp Ile Met Thr Leu Thr Thr Thr Thr Pro Leu Leu Leu Tyr						
145 150 155 160						
AAA GAC CCA GAT AAA GAC TCC ACT CCC GCC ACC TGC CTC AAG ATT TCT						706
Lys Asp Pro Asp Lys Asp Ser Thr Pro Ala Thr Cys Leu Lys Ile Ser						
165 170 175						

099106995 02004

GAC ATC ATC TAT CTA AAA GCT GTG AAC GTG CTG AAC CTC ACT CGA CTG	754
Asp Ile Ile Tyr Leu Lys Ala Val Asn Val Leu Asn Leu Thr Arg Leu	
180 185 190	
ACA TTT TTT TTC TTG ATT CCT TTG TTC ATC ATG ATT GGG TGC TAC TTG	802
Thr Phe Phe Phe Leu Ile Pro Leu Phe Ile Met Ile Gly Cys Tyr Leu	
195 200 205	
GTC ATT ATT CAT AAT CTC CTT CAC GGC AGG ACG TCT AAG CTG AAA CCC	850
Val Ile Ile His Asn Leu Leu His Gly Arg Thr Ser Lys Leu Lys Pro	
210 215 220	
AAA GTC AAG GAG AAG TCC ATA AGG ATC ATC ATC ACG CTG CTG GTG CAG	898
Lys Val Lys Glu Lys Ser Ile Arg Ile Ile Ile Thr Leu Leu Val Gln	
225 230 235 240	
GTG CTC GTC TGC TTT ATG CCC TTC CAC ATC TGT TTC GCT TTC CTG ATG	946
Val Leu Val Cys Phe Met Pro Phe His Ile Cys Phe Ala Phe Leu Met	
245 250 255	
CTG GGA ACG GGG GAG AAC AGT TAC AAT CCC TGG GGA GCC TTT ACC ACC	994
Leu Gly Thr Gly Glu Asn Ser Tyr Asn Pro Trp Gly Ala Phe Thr Thr	
260 265 270	
TTC CTC ATG AAC CTC AGC ACG TGT CTG GAT GTG ATT CTC TAC TAC ATC	1042
Phe Leu Met Asn Leu Ser Thr Cys Leu Asp Val Ile Leu Tyr Tyr Ile	
275 280 285	
GTT TCA AAA CAA TTT CAG GCT CGA GTC ATT AGT GTC ATG CTA TAC CGT	1090
Val Ser Lys Gln Phe Gln Ala Arg Val Ile Ser Val Met Leu Tyr Arg	
290 295 300	
AAT TAC CTT CGA AGC ATG CGC AGA AAA AGT TTC CGA TCT GGT AGT CTA	1138
Asn Tyr Leu Arg Ser Met Arg Arg Lys Ser Phe Arg Ser Gly Ser Leu	
305 310 315 320	
CGG TCA CTA AGC AAT ATA AAC AGT GAA ATG TTA TGAATAATAA GGTTCTTTCA	1191
Arg Ser Leu Ser Asn Ile Asn Ser Glu Met Leu	
325 330	
TTTCAATCCC ATCAAAATTC ACTTCACTAA CTACTCTGGC GTCAATGGAT ATTCTGTATA	1251
ATACTATCAA GTCCCTTTTC TCTTGAAAAA ATAAATTCAT TATCTTCATT TTAAAACTT	1311
AAA	1314

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Ile	Thr	Leu	Asn	Asn	Gln	Asp	Gln	Pro	Val	Pro	Phe	Asn	Ser	Ser
1				5					10					15	
His	Pro	Asp	Glu	Tyr	Lys	Ile	Ala	Ala	Leu	Val	Phe	Tyr	Ser	Cys	Ile
			20					25					30		
Phe	Ile	Ile	Gly	Leu	Phe	Val	Asn	Ile	Thr	Ala	Leu	Trp	Val	Phe	Ser
		35					40					45			
Cys	Thr	Thr	Lys	Lys	Arg	Thr	Thr	Val	Thr	Ile	Tyr	Met	Met	Asn	Val
	50					55					60				
Ala	Leu	Val	Asp	Leu	Ile	Phe	Ile	Met	Thr	Leu	Pro	Phe	Arg	Met	Phe
65					70					75					80
Tyr	Tyr	Ala	Lys	Asp	Ala	Trp	Pro	Phe	Gly	Glu	Tyr	Phe	Cys	Gln	Ile
			85						90					95	
Ile	Gly	Ala	Leu	Thr	Val	Phe	Tyr	Pro	Ser	Ile	Ala	Leu	Trp	Leu	Leu
			100					105					110		
Ala	Phe	Ile	Ser	Ala	Asp	Arg	Tyr	Met	Ala	Ile	Val	Gln	Pro	Lys	Tyr
		115					120					125			
Ala	Lys	Glu	Leu	Lys	Asn	Thr	Cys	Lys	Ala	Val	Leu	Ala	Cys	Val	Gly
	130					135					140				
Val	Trp	Ile	Met	Thr	Leu	Thr	Thr	Thr	Thr	Pro	Leu	Leu	Leu	Leu	Tyr
145					150					155					160
Lys	Asp	Pro	Asp	Lys	Asp	Ser	Thr	Pro	Ala	Thr	Cys	Leu	Lys	Ile	Ser
			165						170					175	
Asp	Ile	Ile	Tyr	Leu	Lys	Ala	Val	Asn	Val	Leu	Asn	Leu	Thr	Arg	Leu
			180					185					190		
Thr	Phe	Phe	Phe	Leu	Ile	Pro	Leu	Phe	Ile	Met	Ile	Gly	Cys	Tyr	Leu
		195					200					205			
Val	Ile	Ile	His	Asn	Leu	Leu	His	Gly	Arg	Thr	Ser	Lys	Leu	Lys	Pro
	210					215					220				
Lys	Val	Lys	Glu	Lys	Ser	Ile	Arg	Ile	Ile	Ile	Thr	Leu	Leu	Val	Gln
225					230					235					240
Val	Leu	Val	Cys	Phe	Met	Pro	Phe	His	Ile	Cys	Phe	Ala	Phe	Leu	Met
				245					250					255	
Leu	Gly	Thr	Gly	Glu	Asn	Ser	Tyr	Asn	Pro	Trp	Gly	Ala	Phe	Thr	Thr
			260					265					270		
Phe	Leu	Met	Asn	Leu	Ser	Thr	Cys	Leu	Asp	Val	Ile	Leu	Tyr	Tyr	Ile
		275					280					285			
Val	Ser	Lys	Gln	Phe	Gln	Ala	Arg	Val	Ile	Ser	Val	Met	Leu	Tyr	Arg
290						295					300				

Asn Tyr Leu Arg Ser Met Arg Arg Lys Ser Phe Arg Ser Gly Ser Leu
305 310 315 320

Arg Ser Leu Ser Asn Ile Asn Ser Glu Met Leu
325 330

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..226

(x) PUBLICATION INFORMATION:

- (H) DOCUMENT NUMBER: US 60/053,693
- (I) FILING DATE: 25-JUL-1997

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

G CTA CAA GGA CAG GAG AAC AGC TAT AGC CCC TGG GGA GCC TTC ACC	46
Leu Gln Gly Gln Glu Asn Ser Tyr Ser Pro Trp Gly Ala Phe Thr	
1 5 10 15	
ACC TTC CTC ATG AAC CTC AGC ACC TGT CTC GAT GTA GTC CTC TAC TAC	94
Thr Phe Leu Met Asn Leu Ser Thr Cys Leu Asp Val Val Leu Tyr Tyr	
20 25 30	
ATC GTT TCC AAA CAG TTC CAG GCT CGA GTC ATC AGC GTC ATG CTG TAC	142
Ile Val Ser Lys Gln Phe Gln Ala Arg Val Ile Ser Val Met Leu Tyr	
35 40 45	
CGC AAT TAC CTT CGC AGT GTT CGC AGA AAA AGT GTC CGA TCG GGC AGT	190
Arg Asn Tyr Leu Arg Ser Val Arg Arg Lys Ser Val Arg Ser Gly Ser	
50 55 60	
TTA CGG TCA CTT AGC AAC ATG AAC AGT GAG ATG CTT TGAGTCAGAG	236
Leu Arg Ser Leu Ser Asn Met Asn Ser Glu Met Leu	
65 70 75	
CAAGCTGCCA GTCTTCAGTC TCTTTAAAAT TCTTTTCCTA TCTACTTTTCG GGTGAACCAG	296
CATTCTACAC TATCCAGTCC CTCTCTAAC AAAGAGAAAT AATAATGATG AACTTTAAAA	356
ACTTCTGCGG TATTCTGTGT ATTCTAGCCA CATGATTAAA AACT	400

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 amino acids

0991069E-07004

(D) OTHER INFORMATION: /note= ""residue 1490 may be A, C, T, or G""

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1495

(D) OTHER INFORMATION: /note= ""residue 1495 may be A or T""

(x) PUBLICATION INFORMATION:

(H) DOCUMENT NUMBER: US 60/053,693

(I) FILING DATE: 25-JUL-1997

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ATTCGGCTTA CTCACTATAG GGCTCGAGCG GCGCCCGGGC AGGTCAAGAC TGCTCCTCTC	60
TGCCGACTAC AACAGATTGG AGCC ATG GCT TTG GAA CAG AAC CAG TCA ACA	111
Met Ala Leu Glu Gln Asn Gln Ser Thr	
1 5	
GAT TAT TAT TAT GAG GAA AAT GAA ATG AAC GGC ACT TAT GAC TAC AGT	159
Asp Tyr Tyr Tyr Glu Glu Asn Glu Met Asn Gly Thr Tyr Asp Tyr Ser	
10 15 20 25	
CAA TAT GAA CTG ATC TGT ATC AAA GAA GAT GTC AGA GAA TTT GCA AAA	207
Gln Tyr Glu Leu Ile Cys Ile Lys Glu Asp Val Arg Glu Phe Ala Lys	
30 35 40	
GTT TTC CTC CCT GTA TTC CTC ACA ATA GTT TTC GTC ATT GGA CTT GCA	255
Val Phe Leu Pro Val Phe Leu Thr Ile Val Phe Val Ile Gly Leu Ala	
45 50 55	
GGC AAT TCC ATG GTA GTG GCA ATT TAT GCC TAT TAC AAG AAA CAG AGA	303
Gly Asn Ser Met Val Val Ala Ile Tyr Ala Tyr Tyr Lys Lys Gln Arg	
60 65 70	
ACC AAA ACA GAT GTG TAC ATC CTG AAT TTG GCT GTA GCA GAT TTA CTC	351
Thr Lys Thr Asp Val Tyr Ile Leu Asn Leu Ala Val Ala Asp Leu Leu	
75 80 85	
CTT CTA TTC ACT CTG CCT TTT TGG GCT GTT AAT GCA GTT CAT GGG TGG	399
Leu Leu Phe Thr Leu Pro Phe Trp Ala Val Asn Ala Val His Gly Trp	
90 95 100 105	
GTT TTA GGG AAA ATA ATG TGC AAA ATA ACT TCA GCC TTG TAC ACA CTA	447
Val Leu Gly Lys Ile Met Cys Lys Ile Thr Ser Ala Leu Tyr Thr Leu	
110 115 120	
AAC TTT GTC TCT GGA ATG CAG TTT CTG GCT TGT ATC AGC ATA GAC AGA	495
Asn Phe Val Ser Gly Met Gln Phe Leu Ala Cys Ile Ser Ile Asp Arg	
125 130 135	
TAT GTG GCA GTA ACT AAA GTC CCC AGC CAA TCA GGA GTG GGA AAA CCA	543
Tyr Val Ala Val Thr Lys Val Pro Ser Gln Ser Gly Val Gly Lys Pro	
140 145 150	
TGC TGG ATC ATC TGT TCC TGT GTC TGG ATG GCT GCC ATC TTG CTG AGC	591

Cys	Trp	Ile	Ile	Cys	Ser	Cys	Val	Trp	Met	Ala	Ala	Ile	Leu	Leu	Ser		
155						160					165						
ATA	CCC	CAG	CTG	GTT	TTT	TAT	ACA	GTA	AAT	GAC	AAT	GCT	AGG	TGC	ATT	639	
Ile	Pro	Gln	Leu	Val	Phe	Tyr	Thr	Val	Asn	Asp	Asn	Ala	Arg	Cys	Ile		
170					175					180					185		
CCC	ATT	TTC	CCC	CGC	TAC	CTA	AGA	ACA	TCA	ATG	AAA	GCA	TTG	ATT	CAA	687	
Pro	Ile	Phe	Pro	Arg	Tyr	Leu	Arg	Thr	Ser	Met	Lys	Ala	Leu	Ile	Gln		
				190					195					200			
ATG	CTA	GAG	ATC	TGC	ATT	GGA	TTT	GTA	GTA	CCC	TTT	CTT	ATT	ATG	GGG	735	
Met	Leu	Glu	Ile	Cys	Ile	Gly	Phe	Val	Val	Pro	Phe	Leu	Ile	Met	Gly		
			205					210					215				
GTG	TGC	TAC	TTT	ATC	ACA	GCA	AGG	ACA	CTC	ATG	AAG	ATG	CCA	AAC	ATT	783	
Val	Cys	Tyr	Phe	Ile	Thr	Ala	Arg	Thr	Leu	Met	Lys	Met	Pro	Asn	Ile		
		220					225					230					
AAA	ATA	TCT	CGA	CCC	CTA	AAA	GTT	CTG	CTC	ACA	GTC	GTT	ATA	GTT	TTC	831	
Lys	Ile	Ser	Arg	Pro	Leu	Lys	Val	Leu	Leu	Thr	Val	Val	Ile	Val	Phe		
	235					240					245						
ATT	GTC	ACT	CAA	CTG	CCT	TAT	AAC	ATT	GTC	AAG	TTC	TGC	CGA	GCC	ATA	879	
Ile	Val	Thr	Gln	Leu	Pro	Tyr	Asn	Ile	Val	Lys	Phe	Cys	Arg	Ala	Ile		
250					255					260					265		
GAC	ATC	ATC	TAC	TCC	CTG	ATC	ACC	AGC	TGC	AAC	ATG	AGC	AAA	CGC	ATG	927	
Asp	Ile	Ile	Tyr	Ser	Leu	Ile	Thr	Ser	Cys	Asn	Met	Ser	Lys	Arg	Met		
				270					275					280			
GAC	ATC	GCC	ATC	CAA	GTC	ACA	GAA	AGC	ATC	GCA	CTC	TTT	CAC	AGC	TGC	975	
Asp	Ile	Ala	Ile	Gln	Val	Thr	Glu	Ser	Ile	Ala	Leu	Phe	His	Ser	Cys		
		285						290					295				
CTC	AAC	CCA	ATC	CTT	TAT	GTT	TTT	ATG	GGA	GCA	TCT	TTC	AAA	AAC	TAC	1023	
Leu	Asn	Pro	Ile	Leu	Tyr	Val	Phe	Met	Gly	Ala	Ser	Phe	Lys	Asn	Tyr		
		300					305					310					
GTT	ATG	AAA	GTG	GCC	AAG	AAA	TAT	GGG	TCC	TGG	AGA	AGA	CAG	AGA	CAA	1071	
Val	Met	Lys	Val	Ala	Lys	Lys	Tyr	Gly	Ser	Trp	Arg	Arg	Gln	Arg	Gln		
	315					320					325						
AGT	GTG	GAG	GAG	TTT	CCT	TTT	GAT	TCT	GAG	GGT	CCT	ACA	GAG	CCA	ACC	1119	
Ser	Val	Glu	Glu	Phe	Pro	Phe	Asp	Ser	Glu	Gly	Pro	Thr	Glu	Pro	Thr		
330					335					340					345		
AGT	ACT	TTT	AGC	ATT	TAAAGGTAAA	ACTGCTCTGC	CTTTTGCTTG	GATACATATG								1174	
Ser	Thr	Phe	Ser	Ile													
				350													
AATGATGCTT	TCCCCTCAAA	TAAAACATCT	GCATTATTCT	GAAACTCAAA	TCTCAGACGC											1234	
CGTGGTTGCA	ACTTATAATA	AAGAATGGGT	TGGGGGAAGG	GGGAGAAATA	AAAGCCAAGA											1294	
AGAAGAAACA	AGATAATAAA	TGTACAAAAC	ATGAAAATTA	AAATGAACAA	TATAGGAAAA											1354	
TAATTGTAAC	AGGCATAAGT	GAATAACACT	CTGCTGTAAC	GAAGAAAAC	TTGTGGTGAT											1414	

AATTTTGTAT CTGTTTGCA GTGGTGCTTA TACCAATCTA CACCAGTGAT AAAATGACCC 1474
 AGAACTATTT CCCCCCTTGT TCCCATTTCA ATTTCTGGT TTTGACATTA TAGTATAATT 1534
 ATGTTAGATG GAACC 1549

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 350 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met	Ala	Leu	Glu	Gln	Asn	Gln	Ser	Thr	Asp	Tyr	Tyr	Tyr	Glu	Glu	Asn	1	5	10	15
Glu	Met	Asn	Gly	Thr	Tyr	Asp	Tyr	Ser	Gln	Tyr	Glu	Leu	Ile	Cys	Ile	20	25	30	
Lys	Glu	Asp	Val	Arg	Glu	Phe	Ala	Lys	Val	Phe	Leu	Pro	Val	Phe	Leu	35	40	45	
Thr	Ile	Val	Phe	Val	Ile	Gly	Leu	Ala	Gly	Asn	Ser	Met	Val	Val	Ala	50	55	60	
Ile	Tyr	Ala	Tyr	Tyr	Lys	Lys	Gln	Arg	Thr	Lys	Thr	Asp	Val	Tyr	Ile	65	70	75	80
Leu	Asn	Leu	Ala	Val	Ala	Asp	Leu	Leu	Leu	Phe	Thr	Leu	Pro	Phe		85	90	95	
Trp	Ala	Val	Asn	Ala	Val	His	Gly	Trp	Val	Leu	Gly	Lys	Ile	Met	Cys	100	105	110	
Lys	Ile	Thr	Ser	Ala	Leu	Tyr	Thr	Leu	Asn	Phe	Val	Ser	Gly	Met	Gln	115	120	125	
Phe	Leu	Ala	Cys	Ile	Ser	Ile	Asp	Arg	Tyr	Val	Ala	Val	Thr	Lys	Val	130	135	140	
Pro	Ser	Gln	Ser	Gly	Val	Gly	Lys	Pro	Cys	Trp	Ile	Ile	Cys	Ser	Cys	145	150	155	160
Val	Trp	Met	Ala	Ala	Ile	Leu	Leu	Ser	Ile	Pro	Gln	Leu	Val	Phe	Tyr	165	170	175	
Thr	Val	Asn	Asp	Asn	Ala	Arg	Cys	Ile	Pro	Ile	Phe	Pro	Arg	Tyr	Leu	180	185	190	
Arg	Thr	Ser	Met	Lys	Ala	Leu	Ile	Gln	Met	Leu	Glu	Ile	Cys	Ile	Gly	195	200	205	

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Phe Val Val Pro Phe Leu Ile Met Gly Val Cys Tyr Phe Ile Thr Ala
 210 215 220
 Arg Thr Leu Met Lys Met Pro Asn Ile Lys Ile Ser Arg Pro Leu Lys
 225 230 235 240
 Val Leu Leu Thr Val Val Ile Val Phe Ile Val Thr Gln Leu Pro Tyr
 245 250 255
 Asn Ile Val Lys Phe Cys Arg Ala Ile Asp Ile Ile Tyr Ser Leu Ile
 260 265 270
 Thr Ser Cys Asn Met Ser Lys Arg Met Asp Ile Ala Ile Gln Val Thr
 275 280 285
 Glu Ser Ile Ala Leu Phe His Ser Cys Leu Asn Pro Ile Leu Tyr Val
 290 295 300
 Phe Met Gly Ala Ser Phe Lys Asn Tyr Val Met Lys Val Ala Lys Lys
 305 310 315 320
 Tyr Gly Ser Trp Arg Arg Gln Arg Gln Ser Val Glu Glu Phe Pro Phe
 325 330 335
 Asp Ser Glu Gly Pro Thr Glu Pro Thr Ser Thr Phe Ser Ile
 340 345 350

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1273 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 429..1238

(x) PUBLICATION INFORMATION:

- (H) DOCUMENT NUMBER: US 60/053,693
- (I) FILING DATE: 25-JUL-1997

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GATGCATGCT CGAGCGGCCG CCAGTGTGAT GGATATCTGC AGAATTCGGC TTACTCACTA	60
TAGGGCTCGA GCGGCCGCCC GGGCAGGTCC CTCCAACAAG ACGCAGCACA GAGACACCAC	120
CTACCTAACA CAGGCGACTC TGAGCACTCT CTCTCTGGGA CTGGGCAGAG CGGCAAACGG	180
TCACCTCTCA GACAGCCTTT GACAGACAGG AGGTTCTACA TACCATGGGA GCCAGCCTGC	240
TGTAAGATGG CCACCCTGAG CAATCACAAC CAGCTTGATC TTTCTAATGG CTCACACCCA	300

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GAGGAATACA AAATCGCAGC CCTAGTCTTC TACAGCTGCA TCTTCCTGAT TGGGCTGTTT	360
GTTAATGTCA CTGCGTTGTG GGTTTTTCAGC TGTACGACCA AGAAAAGAAC ACAGTGACCA	420
TCTACATG ATG AAC GTT GCA CTA CTG GAC CTC GTA TTT ATA CTC AGT CTG	470
Met Asn Val Ala Leu Leu Asp Leu Val Phe Ile Leu Ser Leu	
1 5 10	
CCC TTT CGG ATG TTT TAC TAT GCA AAA GGC GAG TGG CCA TTT GGA GAG	518
Pro Phe Arg Met Phe Tyr Tyr Ala Lys Gly Glu Trp Pro Phe Gly Glu	
15 20 25 30	
TAC TTC TGC CAC ATT CTT GGG GCC CTG GTG GTG TTT TAC CCA AGC CTC	566
Tyr Phe Cys His Ile Leu Gly Ala Leu Val Val Phe Tyr Pro Ser Leu	
35 40 45	
GCT CTG TGG CTT CTT GCT TTC ATT AGT GCT GAC AGA TAC ATG GCC ATC	614
Ala Leu Trp Leu Leu Ala Phe Ile Ser Ala Asp Arg Tyr Met Ala Ile	
50 55 60	
GTA CAG CCA AAA TAT GCC AAG GAG CTG AAG AAC ACC GGC AAG GCC GTG	662
Val Gln Pro Lys Tyr Ala Lys Glu Leu Lys Asn Thr Gly Lys Ala Val	
65 70 75	
CTT GCG TGT GGG GGG GTC TGG GTA ATG ACC CTG ACC ACC ACT GTC CCC	710
Leu Ala Cys Gly Gly Val Trp Val Met Thr Leu Thr Thr Thr Val Pro	
80 85 90	
CTG CTA CTG CTC TAC GAA GAC CCA GAC AAT GCC TCC TCC CCG GCC ACC	758
Leu Leu Leu Leu Tyr Glu Asp Pro Asp Asn Ala Ser Ser Pro Ala Thr	
95 100 105 110	
TGC CTG AAG ATC TCC GAC ATC ACC CAC TTA AAA GCT GTC AAC GTG CTC	806
Cys Leu Lys Ile Ser Asp Ile Thr His Leu Lys Ala Val Asn Val Leu	
115 120 125	
AAC TTC ACG CGA CTC ATA TTT TTC TTC CTG ATC CCT TTG TTC ATC ATG	854
Asn Phe Thr Arg Leu Ile Phe Phe Phe Leu Ile Pro Leu Phe Ile Met	
130 135 140	
ATC GGG TGC TAC GTG GTC ATC ATT CAC AGT CTC CTC CGA GGG CAG ACG	902
Ile Gly Cys Tyr Val Val Ile Ile His Ser Leu Leu Arg Gly Gln Thr	
145 150 155	
TCT AAG CTG AAG CCC AAG GTC AAG GAG AAG TCC ATA CGG ATC ATC ATG	950
Ser Lys Leu Lys Pro Lys Val Lys Glu Lys Ser Ile Arg Ile Ile Met	
160 165 170	
ACC CTC CTG CTG CAG GTG CTC GTC TGC TTC GTG CCC TTC CAC ATC TGC	998
Thr Leu Leu Leu Gln Val Leu Val Cys Phe Val Pro Phe His Ile Cys	
175 180 185 190	
TTT GCC GTC CTG ATG CTA CAA GGA CAG GAG AAC AGC TAT AGC CCC TGG	1046
Phe Ala Val Leu Met Leu Gln Gly Gln Glu Asn Ser Tyr Ser Pro Trp	
195 200 205	
GGA GCC TTC ACC ACC TTC CTC ATG AAC CTC AGC ACC TGT CTC GAT GTA	1094
Gly Ala Phe Thr Thr Phe Leu Met Asn Leu Ser Thr Cys Leu Asp Val	

210										215					220					
GTC	CTC	TAC	TAC	ATC	GTT	TCC	AAA	CAG	TTC	CAG	GCT	CGA	GTC	ATC	AGC	1142				
Val	Leu	Tyr	Tyr	Ile	Val	Ser	Lys	Gln	Phe	Gln	Ala	Arg	Val	Ile	Ser					
		225					230					235								
GTC	ATG	CTG	TAC	CGC	AAT	TAC	CTT	CGC	AGT	GTT	CGC	AGA	AAA	AGT	GTC	1190				
Val	Met	Leu	Tyr	Arg	Asn	Tyr	Leu	Arg	Ser	Val	Arg	Arg	Lys	Ser	Val					
	240					245					250									
CGA	TCG	GGC	AGT	TTA	CGG	TCA	CTT	AGC	AAC	ATG	AAC	AGT	GAG	ATG	CTT	1238				
Arg	Ser	Gly	Ser	Leu	Arg	Ser	Leu	Ser	Asn	Met	Asn	Ser	Glu	Met	Leu					
255					260					265				270						
TGAGTCAGAG CAAGCTGCCA GTCTTCAGTC TCTTT															1273					

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met	Asn	Val	Ala	Leu	Leu	Asp	Leu	Val	Phe	Ile	Leu	Ser	Leu	Pro	Phe
1				5					10					15	
Arg	Met	Phe	Tyr	Tyr	Ala	Lys	Gly	Glu	Trp	Pro	Phe	Gly	Glu	Tyr	Phe
			20					25					30		
Cys	His	Ile	Leu	Gly	Ala	Leu	Val	Val	Phe	Tyr	Pro	Ser	Leu	Ala	Leu
			35				40					45			
Trp	Leu	Leu	Ala	Phe	Ile	Ser	Ala	Asp	Arg	Tyr	Met	Ala	Ile	Val	Gln
	50					55					60				
Pro	Lys	Tyr	Ala	Lys	Glu	Leu	Lys	Asn	Thr	Gly	Lys	Ala	Val	Leu	Ala
	65				70					75				80	
Cys	Gly	Gly	Val	Trp	Val	Met	Thr	Leu	Thr	Thr	Thr	Val	Pro	Leu	Leu
			85					90						95	
Leu	Leu	Tyr	Glu	Asp	Pro	Asp	Asn	Ala	Ser	Ser	Pro	Ala	Thr	Cys	Leu
			100				105						110		
Lys	Ile	Ser	Asp	Ile	Thr	His	Leu	Lys	Ala	Val	Asn	Val	Leu	Asn	Phe
			115				120					125			
Thr	Arg	Leu	Ile	Phe	Phe	Phe	Leu	Ile	Pro	Leu	Phe	Ile	Met	Ile	Gly
	130						135					140			
Cys	Tyr	Val	Val	Ile	Ile	His	Ser	Leu	Leu	Arg	Gly	Gln	Thr	Ser	Lys
145					150					155					160

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Leu	Lys	Pro	Lys	Val	Lys	Glu	Lys	Ser	Ile	Arg	Ile	Ile	Met	Thr	Leu
				165					170					175	
Leu	Leu	Gln	Val	Leu	Val	Cys	Phe	Val	Pro	Phe	His	Ile	Cys	Phe	Ala
			180					185					190		
Val	Leu	Met	Leu	Gln	Gly	Gln	Glu	Asn	Ser	Tyr	Ser	Pro	Trp	Gly	Ala
		195					200					205			
Phe	Thr	Thr	Phe	Leu	Met	Asn	Leu	Ser	Thr	Cys	Leu	Asp	Val	Val	Leu
	210					215					220				
Tyr	Tyr	Ile	Val	Ser	Lys	Gln	Phe	Gln	Ala	Arg	Val	Ile	Ser	Val	Met
225					230					235					240
Leu	Tyr	Arg	Asn	Tyr	Leu	Arg	Ser	Val	Arg	Arg	Lys	Ser	Val	Arg	Ser
				245					250					255	
Gly	Ser	Leu	Arg	Ser	Leu	Ser	Asn	Met	Asn	Ser	Glu	Met	Leu		
			260					265					270		

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